SPECIFICATION AMENDMENTS

Please amend the specification as follows:

Abstract

The invention provides methods and compositions related to transgenic plants which incorporate genetic traits of the marine eelgrass *Zostera marina*. These traits include pathogen resistance, which may be conferred by stimulating zosteric acid biosynthesis~~, and root anoxia resistance, which may be conferred by introducing one or more anoxia-induced or anoxia-resistance genes~~.

Brief Description of the Figures

Figure 1 depicts a pathway for zosteric acid biosynthesis.

Figure 2 depicts the basic steps involved in cloning and expressing sulfotransferase (ST) from *Zostera marina*.

Figure 3 depicts the degenerate (SEQ ID NO: 5 - 7) and gene-specific primers used in cloning *Zostera marina* sulfotransferase. Amino acid sequences corresponding to the degenerate sequences are indicated by SEQ ID NO: 12-14.

Figure 4 depicts the nucleotide and amino acid sequence of a ~~cDNA clone of~~ sulfotransferase cloned from *Zostera marina* (SEQ ID NO: 15 and 16).

Figure 5 depicts an alignment of the deduced *Zostera marina* sulfotransferase amino acid sequence (SEQ ID NO: 17) with sulfotransferases from *Arabidopsis thaliana* (P52839)(SEQ ID NO: 19), *Brassica napus* (T07832) (SEQ ID NO: 18), *Flaveria bidentis* (P52832) (SEQ ID NO: 20) and *Homo sapiens* (NM003166) (SEQ ID NO: 21). The arrowed lines indicate the location of the conserved blocks and the dots indicate the motif involved in dimerization of the enzymes. The sequences were aligned using MegAlign program from DNAStar Inc.

Figure 6 depicts the sequence of the intron from *Zostera marina* sulfotransferase (SEQ ID NO: 22). Sequences inside the boxes are consensus motifs of the 5' and 3' intron splice sites for plant genes. Stop codons are indicated by the dots.

Figure 7 depicts a method of identifying the function of the *Zostera marina* ST gene product through subcloning, expression and enzymic activity analysis.

Figure 8 depicts an ST-catalyzed sulfur transferation reaction assay.

Figure 9 depicts purification of the ST by the ST-catalyzed sulfur transferation reaction assay.

Figure 10 summarizes a comparison of *Zostera marina*, Flaveria and Rat Dopa/tyrosine ST activities.

Figure 11 depicts the sequences of degenerate primers to conserved protein sequences of ADH (SEQ ID NO: 23 and 29), CH (SEQ ID NO: 24 and 30) and PAL (SEQ ID NO: 25 and 31) used in cloning *Zostera marina* Alcohol Dehydrogenase, Cinnamate 4-Hydroxylase and Phenylalanine Ammonia Lyase genes from *Zostera marina.*

Figure 12 summarizes the approximate sizes of the ADH, CH, PAL and POX targeted genes and the size of the of partial clone obtained.

Figure 13 depicts the nucleotide and amino acid sequence of a partial alcohol dehydrogenase cDNA clone from *Zostera marina* (SEQ ID NO: 35 and SEQ ID NO: 36).

Figure 14 depicts an alignment of the deduced *Zostera marina* ADH amino acid sequence (SEQ ID NO: 37) with ~~*Arabisopsis*~~ *Arabidopsis thaliana* ADH (BAA 19623) (SEQ ID NO: 38), corn (S04571) (SEQ ID NO: 39), and *E. coli* (AAC73459) (SEQ ID NO: 40).

Figure 15 depicts the nucleotide and amino acid sequence of a partial cinnamate 4-hydroxylase cDNA clone from *Zostera marina* (SEQ ID NO: 41 and SEQ ID NO: 42).

Figure 16 depicts an alignment of the deduced *Zostera marina* CH amino acid sequence (SEQ ID NO: 43) with *Citrus senensis* CH (AAF66066) (SEQ ID NO: 44) and *Phaseolus vulgaris* (Kidney Bean) CH (T10857) (SEQ ID NO: 45).

Figure 17 depicts the nucleotide and amino acid sequence of a partial Phenylalanine ammonia lyase cDNA clone from *Zostera marina* (SEQ ID NO: 46 and SEQ ID NO: 47).

Figure 18 depicts an alignment of the deduced *Zostera marina* PAL amino acid sequence (SEQ ID NO: 48) with *Arabidopsis thaliana* PAL (S52991) (SEQ ID NO: 49) and *Triticum aestivum* (wheat) PAL (CAA68036) (SEQ ID NO: 50).

Figure 19 depicts several steps in fungal infection which may be targeted by one or more of the transgenic strategies of the invention.~~an alignment of the deduced *Zostera marina* PAL amino acid sequence with *Arabidopsis thaliana* PAL (S52991) and *Triticum aestivum* (wheat) PAL (CAA68036).~~

Figure 20 shows ~~microscopically~~ micrographs depicting the infection process for *Colletotrichum.*

Figure 21 (A, B) summarizes a number of known plant pathogenic fungi, the popular names of the diseases they cause, and the crop plant types that they infect.

Figure 22 summarizes some of the results obtained to date using various fungal pathogens.

Figure 23 shows that *Epifend* inhibits adhesion of *Colletotrichum* spores to polystyrene, while coumaric acid did not inhibit spore adhesion.

Figure 24 shows that *Epifend* inhibits spore adhesion to glass, polystyrene and leaf surfaces, at concentrations as low as 0.01%.

Figure 25 depicts the infection of rice blast by *Magnaporthe grisea.*

Figure 26 shows that *Epifend* inhibits spore adhesion to polystyrene and rice leaf surfaces, at concentrations as low as 0.01%.

Figure 27 shows that *Epifend* -treated rice leaf had ungerminated spores.

Figure 28 depicts a rice leaf spot assay in which *Epifend* (at 0.2%) fully prevents lesion formation.

Figure 29 shows the effect of 1% *Epifend* in reducing infection in Bintje (at 4 days).

Figure 30 shows the effect of 1% *Epifend* in reducing infection in Bintje (at 11 days).